Introduction to Computer Methods in Molecular Structure

The objective of this set of lectures and laboratories is to provide students with a basic knowledge about some of the computational resources related to studies in the field of computational biology, and to enable them to use some of these tools.



Overview

- Molecular Graphics Software
 - for publication, visual presentation, and analysis
- Structure and Dynamics Prediction
 - needed for understanding function in
 - protein chemistry
 - protein DNA interactions
 - protein ligand binding
 - intelligent structure based drug design



Molecular Graphics Software

- Rasmol/Raswin
 - for viewing protein structures and producing publication figures
- Protein Explorer
 - uses Rasmol in a user-friendly wrapper
- VMD (Visual Molecular Dynamics)
 - for viewing and analysing molecular dynamics simulations and building dynamics movies

Structure and Dynamics Prediction

- Protein structure and prediction
 - X-ray and neutron diffraction, and NMR, provide experimentally known 3D structures.
 - Ab initio: Go to 3D structure from sequence only.
 - Comparative modeling (comparisons to knowns).
- Prediction of dynamic (function) properties
 - Can use known 3D structures
 - Quantum Mechanics (QM)
 - Molecular Mechanics (MM)



Quantum Mechanics

- required for covalent bond breakingmaking
- first principles approximate solutions to the Schrödinger wave equation, ab initio
- not practical for large proteins, expensive
- used to calculate parameters for Molecular Mechanics potential functions (see below)
- used in combined QM/MM methods large proteins (Gaussian ONIOM)

Molecular Mechanics

- not useful for making and breaking bonds
- calculates molecular energy using classical potential functions with theoretical (from QM) and empirical parameters
- There are many MM force fields available.
- used to refine predictions of 3D structure in
 - Modeler

